



SEQUENCE LISTING

<110> Mount Sinai School of Medicine of NYU

<120> TRP8, A TRANSIENT RECEPTOR POTENTIAL
CHANNEL EXPRESSED IN TASTE RECEPTOR CELL

<130> 1270-007

<140> 09/834,792

<141> 2001-04-13

<150> 60/197,491

<151> 2000-04-17

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4157

<212> DNA

<213> Murine TRP8 cDNA

<400> 1

cagctacatg	ccattaatct	ggaaggaacg	ggcaggaaag	ccaccatgca	aacaacccag	60
agctcctgcc	ccggcagccc	cccagatact	gaggatggct	gggagcccat	cctatgcagg	120
ggagagatca	acttcggagg	gtctgggaag	aagcgaggca	agtttgtgaa	ggtgccaagc	180
agtgtggccc	cctctgtgct	ttttgaactc	ctgctcaccg	agtggcacct	gccagccccc	240
aacctgggtg	tgctcctggt	gggtgaggaa	cgacctttgg	ctatgaagtc	gtggcttcgg	300
gatgtcctgc	gcaaggggct	ggtgaaaagca	gctcagagca	caggtgcctg	gacccctgacc	360
agtgcctctc	acgtgggcct	ggcccgcctc	gttggaacaag	ctgtacgtga	tactctctctg	420
gctagcacat	ccaccaagat	ccgtgtagtg	gccatcgga	tgccctctct	ggatcgaatc	480
cttcaccgtc	aacttctaga	tgggtgtccac	caaaaggagg	atactcccat	ccactaccca	540
gcagatgagg	gcaacattca	gggaccctct	tgcccccctg	acagcaatct	ctcccacttc	600
atccttgtgg	agtcaggcgc	ccttggggagt	gggaacgacg	ggctgacaga	gctgcagctg	660
agcctggaga	agcacatctc	tcagcagagg	acaggttatg	ggggcaccag	ctgcatccag	720
atacctgtcc	tttgccctgtt	ggtcaatggt	gaccccaaca	ccctagagag	gatttccagg	780
gcagtggagc	aggctgcccc	atggctgac	ctggcagggt	ctgggtggcat	tgctgatgta	840
ctcgtgccc	tgggtagcca	gcctcatctc	ctggtgcccc	aggtggctga	gaagcagttc	900
agagagaaat	ccccagcga	gtgtttctct	tgggaagcca	ttgtacactg	gacagagctg	960
ttacagaaca	ttgctgcaca	ccccacctg	ctcacagtat	atgacttcga	gcaggagggt	1020
tcggaggacc	tggacactgt	catcctcaag	gcacttgtga	aagcctgcaa	gagccacagc	1080
caagaagccc	aagactacct	agatgagctc	aagtttagcag	tggcctggga	tcgcgtggac	1140
attgccaaaga	gtgaaatctt	caatggggac	gtggaatgga	agtcctgtga	cttggaagag	1200
gtgatgacag	atgcctctgt	gagcaacaag	cctgactttg	tccgcctctt	tgtggacagc	1260
ggtgctgaca	tggccgagtt	cttgacctat	gggcggtgc	agcagcttta	ccattctgtg	1320
tcccccaaga	gcctcctctt	tgaactgctg	cagcgtaagc	atgaggaggg	taggctgaca	1380
ctggccggcc	tgggtgcccc	gcaggctcgg	gagctgcccc	ttggtctgcc	tgccctctca	1440
ctccacgagg	tctcccgctg	actcaaagac	ttcctgcatg	acgcctgccg	tggcttctac	1500
caggacgggc	gcaggatgga	ggagagaggg	ccacctaaagc	ggcccgaggg	ccagaagtgg	1560
ctgccagacc	tcagtaggaa	gagtgaagac	ccttggaggg	acctgttctt	ctgggctgtg	1620
ctgcagaatc	gttatgagat	ggccacatac	ttctgggcca	tgggcccggga	gggtgtggct	1680
gctgctctgg	ctgcctgcaa	gatcataaag	gaaatgtccc	acctggagaa	agaggcagag	1740
gtggcccgc	ccatgcgtga	ggccaagtat	gagcagctgg	ccctggatct	tttctcagag	1800
tgctacggca	acagtgagga	ccgtgccttt	gccctgctgg	tgccaaggaa	ccacagctgg	1860

```

agcaggacca cgtgçctgca cctggccact` gaagctgatg ccaaggcctt ctttgcccat 1920
gacgggtgtgc aagcattcct gaccaagatc tgggtggggag acatggccac aggcacaccc 1980
atcctacggc ttctgggtgc cttcacctgc ccagccctca tctacacaaa cctcatctcc 2040
ttcagtgagg atgccccgca gaggatggac ctagaagatc tgcaggagcc agacagcttg 2100
gatatggaaa agagcttcct atgcagccgg ggtggccaat tggagaagct aacagaggca 2160
ccaagggctc caggcgatct agggccacaa gctgccttcc tgcacacacg gtggaggaag 2220
ttctggggcg ctctgtgac tgtgttcctg gggaaatgtgg tcatgtactt cgcattcctc 2280
ttcctgttca cctatgtcct gctgggtggac ttcaggccac caccacaggg gccgtctgga 2340
tccgaggtta ccctctattt ctgggtgttc acactgggtg tggaggaaat ccgacagggc 2400
ttcttcacag atgaggacac gcacctggtg aagaaattca ctctgtatgt ggaagacaac 2460
tggaacaagt gtgacatggt ggccatcttc ctgttcattg tgggagtcac ctgtagaatg 2520
gtgcctcgg tgtttgaggc tggcaggacc gttctggcca ttgacttcat ggtgttcaca 2580
cttcggctca tccacatctt tgctattcac aagcagttgg gtccctaagat catcattgta 2640
gagcgaatga tgaaggatgt cttctttttc ctcttcttcc tgagcgtatg gcttgtggcc 2700
tatggtgtga ccactcaggc cctgctgcat ccccatgatg gccgtttgga gtggattttc 2760
cgccgtgtgc tatacaggcc ttacctgcag atctttgggc aaatccctct ggatgaaatt 2820
gatgaggctc gtgtgaactg ttctcttcac cctctgctgc tggaaagctc ggcttcctgc 2880
cctaattctc atgccaaactg gctggtcatt ctctgctgg ttaccttctc gcttgtcact 2940
aatgtgctgc tcatgaacct tctgatcgcc atgttcagct acacattcca ggtgggtgcaa 3000
ggcaatgcag acatgttctg gaagtttcaa cgctaccacc tcatcgttga ataccatgga 3060
agaccagctc tggccccgcc cttcatcctg ctacgccacc tgagcctggt gctcaagcag 3120
gtcttcagga aggaagccca gcataagcga caacatctgg agagagactt gcctgacccc 3180
ttggaccaga agatcattac ctgggaaacg gttcaaaagg agaacttctc gagtaccatg 3240
gagaaacgga ggagggacag cgagggggag gtgctgagga aaacggcaca cagagtggac 3300
ttgattgcca aatacatcgg ggggctgaga gagcaagaaa agaggatcaa gtgtctggaa 3360
tcacaggcca actactgtat gctcctcttg tctctatga cggatacact ggctccagga 3420
ggcacctact caagctctca gaactgtggt tgcaggagtc agccagcctc tgctagagac 3480
agggagtacc tagagtctgg cttgccaccc tctgacacct gaaatggaga aaccacttgc 3540
tctagagccc cagacctggc cacatcgagt ttttggggca catcaacctt cccccactcc 3600
cagcagcccc aagaaatggt cttcaaggcc ttgtacaga tcaacttctg gacatccctt 3660
cctaagagaa tgaaactcat gtctttggca tctattcggg agcctcagaa gtatcctctc 3720
cagcaggcca agatttttca tgtcccacta aagctttcac tggcttgga tggacagctg 3780
gatctggcca agtctacat aggacaccat ctgcctggat ggggctattt aggtctaacc 3840
cctgtcttac cctgagttcc taagaagcca acctcttaa cactaggttt ctttctgacc 3900
cctgaccac tcatagctg accagctcct agagggcagg actcagatct attgtaatta 3960
cctcccatct ttcaccccc acagcattat ctgtctgatc attctggcag aaaccccaag 4020
atattgctca agggtagccca atgctacttt actttctata aagcctgtag accacctcaa 4080
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4140
aaaaaaaaaa aaaaaaa 4157

```

```

<210> 2
<211> 1158
<212> PRT
<213> Murine TRP8

```

```

<400> 2

```

```

Met Gln Thr Thr Gln Ser Ser Cys Pro Gly Ser Pro Pro Asp Thr Glu
 1           5           10           15
Asp Gly Trp Glu Pro Ile Leu Cys Arg Gly Glu Ile Asn Phe Gly Gly
          20           25           30
Ser Gly Lys Lys Arg Gly Lys Phe Val Lys Val Pro Ser Ser Val Ala
          35           40           45
Pro Ser Val Leu Phe Glu Leu Leu Thr Glu Trp His Leu Pro Ala
          50           55           60

```

Pro	Asn	Leu	Val	Val	Ser	Leu	Val	Gly	Glu	Glu	Arg	Pro	Leu	Ala	Met
65					70					75					80
Lys	Ser	Trp	Leu	Arg	Asp	Val	Leu	Arg	Lys	Gly	Leu	Val	Lys	Ala	Ala
				85					90					95	
Gln	Ser	Thr	Gly	Ala	Trp	Ile	Leu	Thr	Ser	Ala	Leu	His	Val	Gly	Leu
			100					105					110		
Ala	Arg	His	Val	Gly	Gln	Ala	Val	Arg	Asp	His	Ser	Leu	Ala	Ser	Thr
		115					120					125			
Ser	Thr	Lys	Ile	Arg	Val	Val	Ala	Ile	Gly	Met	Ala	Ser	Leu	Asp	Arg
	130					135					140				
Ile	Leu	His	Arg	Gln	Leu	Leu	Asp	Gly	Val	His	Gln	Lys	Glu	Asp	Thr
145					150					155					160
Pro	Ile	His	Tyr	Pro	Ala	Asp	Glu	Gly	Asn	Ile	Gln	Gly	Pro	Leu	Cys
				165					170					175	
Pro	Leu	Asp	Ser	Asn	Leu	Ser	His	Phe	Ile	Leu	Val	Glu	Ser	Gly	Ala
			180					185					190		
Leu	Gly	Ser	Gly	Asn	Asp	Gly	Leu	Thr	Glu	Leu	Gln	Leu	Ser	Leu	Glu
		195				200						205			
Lys	His	Ile	Ser	Gln	Gln	Arg	Thr	Gly	Tyr	Gly	Gly	Thr	Ser	Cys	Ile
	210					215						220			
Gln	Ile	Pro	Val	Leu	Cys	Leu	Leu	Val	Asn	Gly	Asp	Pro	Asn	Thr	Leu
225					230					235					240
Glu	Arg	Ile	Ser	Arg	Ala	Val	Glu	Gln	Ala	Ala	Pro	Trp	Leu	Ile	Leu
				245					250					255	
Ala	Gly	Ser	Gly	Gly	Ile	Ala	Asp	Val	Leu	Ala	Ala	Leu	Val	Ser	Gln
			260				265						270		
Pro	His	Leu	Leu	Val	Pro	Gln	Val	Ala	Glu	Lys	Gln	Phe	Arg	Glu	Lys
		275					280					285			
Phe	Pro	Ser	Glu	Cys	Phe	Ser	Trp	Glu	Ala	Ile	Val	His	Trp	Thr	Glu
	290					295					300				
Leu	Leu	Gln	Asn	Ile	Ala	Ala	His	Pro	His	Leu	Leu	Thr	Val	Tyr	Asp
305					310					315					320
Phe	Glu	Gln	Glu	Gly	Ser	Glu	Asp	Leu	Asp	Thr	Val	Ile	Leu	Lys	Ala
				325					330					335	
Leu	Val	Lys	Ala	Cys	Lys	Ser	His	Ser	Gln	Glu	Ala	Gln	Asp	Tyr	Leu
			340					345					350		
Asp	Glu	Leu	Lys	Leu	Ala	Val	Ala	Trp	Asp	Arg	Val	Asp	Ile	Ala	Lys
		355					360					365			
Ser	Glu	Ile	Phe	Asn	Gly	Asp	Val	Glu	Trp	Lys	Ser	Cys	Asp	Leu	Glu
	370					375					380				
Glu	Val	Met	Thr	Asp	Ala	Leu	Val	Ser	Asn	Lys	Pro	Asp	Phe	Val	Arg
385					390					395					400
Leu	Phe	Val	Asp	Ser	Gly	Ala	Asp	Met	Ala	Glu	Phe	Leu	Thr	Tyr	Gly
				405					410					415	
Arg	Leu	Gln	Gln	Leu	Tyr	His	Ser	Val	Ser	Pro	Lys	Ser	Leu	Leu	Phe
			420					425					430		
Glu	Leu	Leu	Gln	Arg	Lys	His	Glu	Glu	Gly	Arg	Leu	Thr	Leu	Ala	Gly
		435					440					445			
Leu	Gly	Ala	Gln	Gln	Ala	Arg	Glu	Leu	Pro	Ile	Gly	Leu	Pro	Ala	Phe
	450					455					460				
Ser	Leu	His	Glu	Val	Ser	Arg	Val	Leu	Lys	Asp	Phe	Leu	His	Asp	Ala
465					470					475					480
Cys	Arg	Gly	Phe	Tyr	Gln	Asp	Gly	Arg	Arg	Met	Glu	Glu	Arg	Gly	Pro
				485					490					495	
Pro	Lys	Arg	Pro	Ala	Gly	Gln	Lys	Trp	Leu	Pro	Asp	Leu	Ser	Arg	Lys
			500					505					510		
Ser	Glu	Asp	Pro	Trp	Arg	Asp	Leu	Phe	Leu	Trp	Ala	Val	Leu	Gln	Asn

		515					520				525						
Arg	Tyr	Glu	Met	Ala	Thr	Tyr	Phe	Trp	Ala	Met	Gly	Arg	Glu	Gly	Val		
	530					535					540						
Ala	Ala	Ala	Leu	Ala	Ala	Cys	Lys	Ile	Ile	Lys	Glu	Met	Ser	His	Leu		
545					550					555					560		
Glu	Lys	Glu	Ala	Glu	Val	Ala	Arg	Thr	Met	Arg	Glu	Ala	Lys	Tyr	Glu		
				565					570						575		
Gln	Leu	Ala	Leu	Asp	Leu	Phe	Ser	Glu	Cys	Tyr	Gly	Asn	Ser	Glu	Asp		
			580					585						590			
Arg	Ala	Phe	Ala	Leu	Leu	Val	Arg	Arg	Asn	His	Ser	Trp	Ser	Arg	Thr		
		595					600							605			
Thr	Cys	Leu	His	Leu	Ala	Thr	Glu	Ala	Asp	Ala	Lys	Ala	Phe	Phe	Ala		
	610					615								620			
His	Asp	Gly	Val	Gln	Ala	Phe	Leu	Thr	Lys	Ile	Trp	Trp	Gly	Asp	Met		
625					630					635					640		
Ala	Thr	Gly	Thr	Pro	Ile	Leu	Arg	Leu	Leu	Gly	Ala	Phe	Thr	Cys	Pro		
				645					650						655		
Ala	Leu	Ile	Tyr	Thr	Asn	Leu	Ile	Ser	Phe	Ser	Glu	Asp	Ala	Pro	Gln		
			660					665						670			
Arg	Met	Asp	Leu	Glu	Asp	Leu	Gln	Glu	Pro	Asp	Ser	Leu	Asp	Met	Glu		
		675					680							685			
Lys	Ser	Phe	Leu	Cys	Ser	Arg	Gly	Gly	Gln	Leu	Glu	Lys	Leu	Thr	Glu		
	690					695					700						
Ala	Pro	Arg	Ala	Pro	Gly	Asp	Leu	Gly	Pro	Gln	Ala	Ala	Phe	Leu	Leu		
705					710					715					720		
Thr	Arg	Trp	Arg	Lys	Phe	Trp	Gly	Ala	Pro	Val	Thr	Val	Phe	Leu	Gly		
				725				730							735		
Asn	Val	Val	Met	Tyr	Phe	Ala	Phe	Leu	Phe	Leu	Phe	Thr	Tyr	Val	Leu		
			740				745							750			
Leu	Val	Asp	Phe	Arg	Pro	Pro	Pro	Gln	Gly	Pro	Ser	Gly	Ser	Glu	Val		
		755					760							765			
Thr	Leu	Tyr	Phe	Trp	Val	Phe	Thr	Leu	Val	Leu	Glu	Glu	Ile	Arg	Gln		
	770					775					780						
Gly	Phe	Phe	Thr	Asp	Glu	Asp	Thr	His	Leu	Val	Lys	Lys	Phe	Thr	Leu		
785					790					795					800		
Tyr	Val	Glu	Asp	Asn	Trp	Asn	Lys	Cys	Asp	Met	Val	Ala	Ile	Phe	Leu		
				805					810						815		
Phe	Ile	Val	Gly	Val	Thr	Cys	Arg	Met	Val	Pro	Ser	Val	Phe	Glu	Ala		
			820					825						830			
Gly	Arg	Thr	Val	Leu	Ala	Ile	Asp	Phe	Met	Val	Phe	Thr	Leu	Arg	Leu		
		835					840							845			
Ile	His	Ile	Phe	Ala	Ile	His	Lys	Gln	Leu	Gly	Pro	Lys	Ile	Ile	Ile		
	850					855								860			
Val	Glu	Arg	Met	Met	Lys	Asp	Val	Phe	Phe	Phe	Leu	Phe	Phe	Leu	Ser		
865					870					875					880		
Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Thr	Thr	Gln	Ala	Leu	Leu	His	Pro		
				885					890						895		
His	Asp	Gly	Arg	Leu	Glu	Trp	Ile	Phe	Arg	Arg	Val	Leu	Tyr	Arg	Pro		
		900						905						910			
Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro	Leu	Asp	Glu	Ile	Asp	Glu	Ala		
		915					920							925			
Arg	Val	Asn	Cys	Ser	Leu	His	Pro	Leu	Leu	Leu	Glu	Ser	Ser	Ala	Ser		
	930					935								940			
Cys	Pro	Asn	Leu	Tyr	Ala	Asn	Trp	Leu	Val	Ile	Leu	Leu	Leu	Val	Thr		
945					950					955					960		
Phe	Leu	Leu	Val	Thr	Asn	Val	Leu	Leu	Met	Asn	Leu	Leu	Ile	Ala	Met		
				965					970						975		

Phe Ser Tyr Thr Phe Gln Val Val Gln Gly Asn Ala Asp Met Phe Trp
 980 985 990
 Lys Phe Gln Arg Tyr His Leu Ile Val Glu Tyr His Gly Arg Pro Ala
 995 1000 1005
 Leu Ala Pro Pro Phe Ile Leu Leu Ser His Leu Ser Leu Val Leu Lys
 1010 1015 1020
 Gln Val Phe Arg Lys Glu Ala Gln His Lys Arg Gln His Leu Glu Arg
 1025 1030 1035 1040
 Asp Leu Pro Asp Pro Leu Asp Gln Lys Ile Ile Thr Trp Glu Thr Val
 1045 1050 1055
 Gln Lys Glu Asn Phe Leu Ser Thr Met Glu Lys Arg Arg Arg Asp Ser
 1060 1065 1070
 Glu Gly Glu Val Leu Arg Lys Thr Ala His Arg Val Asp Leu Ile Ala
 1075 1080 1085
 Lys Tyr Ile Gly Gly Leu Arg Glu Gln Glu Lys Arg Ile Lys Cys Leu
 1090 1095 1100
 Glu Ser Gln Ala Asn Tyr Cys Met Leu Leu Leu Ser Ser Met Thr Asp
 1105 1110 1115 1120
 Thr Leu Ala Pro Gly Gly Thr Tyr Ser Ser Ser Gln Asn Cys Gly Cys
 1125 1130 1135
 Arg Ser Gln Pro Ala Ser Ala Arg Asp Arg Glu Tyr Leu Glu Ser Gly
 1140 1145 1150
 Leu Pro Pro Ser Asp Thr
 1155

<210> 3

<211> 3498

<212> DNA

<213> Human TRP8 CDNA

<400> 3

atgcaggatg tccaaggccc ccggtcccga agccccggg atgctgaaga ccggcgggag 60
 ctgggcttgc acagggggcga ggtcaacttt ggagggtctg ggaagaagcg aggcaagtgt 120
 gtacgggtgc cgagcggagt ggccccgtct gtgctctttg acctgctgct tgctgagtgg 180
 cacctgccgg cccccaacct ggtggtgtcc ctgggtgggtg aggagcagcc ttctgccatg 240
 aagtccctggc tgcgggatgt gctgcgcaag gggctggtga aggcggctca gacacagga 300
 gcctggatcc tgaccagtgc cctccgcgtg ggccctggcca ggcatgtcgg gcaggccgtg 360
 cgcgaccact cgctggccag cacgtccacc aaggtccgtg tggttgctgt cggcatggcc 420
 tcgctggggc gcgtcctgca ccgccgcatt ctggaggagg cccaggagga ttttcctgtc 480
 cactaccctg aggatgacgg cggcagccag ggccccctct gtctactgga cagcaacctc 540
 tcccacttca tcctggtgga gccaggcccc ccggggaagg gcgatgggct gacggagctg 600
 cggctgagggc tggagaagca catctcggag cagagggcgg gctacggggg cactggcagc 660
 atcgagatcc ctgtcctctg cttgctggtc aatggtgata ccaacacctt ggagaggatc 720
 tccaggggccg tggagcaggc tgccccgtgg ctgactctgg taggctcggg gggcatcgcc 780
 gatgtgcttg ctgccctagt gaaccagccc cactccttgg tgcccaagggt ggccgagaag 840
 cagtttaagg agaagttccc cagcaagcat ttctcttggg aggacatcgt gcgctggacc 900
 aagctgctgc agaacatcac ctacacaccag cacctgctca ccgtgtatga cttcgagcag 960
 gagggtcccg aggagctgga cacgggtcatc ctgaaggcgc tgggtgaaagc ctgcaagagc 1020
 cacagccagg agcctcagga ctatctggat gagctcaagc tggccgtggc ctgggaccgc 1080
 gtggacatcg ccaagagtga gatcttcaat ggggacgtgg agtggaagtc ctgtgacctg 1140
 gaggaggtga tgggtggacgc cctgggtcagc aacaagcccg agtttgtgcg cctcttttgtg 1200
 gacaacggcg cagacgtggc cgacttcctg acgtatgggc ggctgcagga gctctaccgc 1260
 tccgtgtcac gcaagagcct gctcttcgac ctgctgcagc ggaagcagga ggaggcccgg 1320

```

ctgacgctgg cgggctggg caccagcag gcccgggagc caccgcggg gccaccggcc 1380
ttctccctgc acgaggtctc ccgcgtactc aaggacttcc tgcaggacgc ctgccgaggc 1440
ttctaccagg acggccggcc aggggaccgc agggggcgg agaagggcc ggccaagcgg 1500
cccacgggcc agaagtggct gctggacctg aaccagaaga gcgagaacct ctggcgggac 1560
ctgttcctgt gggcctgtgt gcagaaccgc cacgagatgg ccacctactt ctgggccatg 1620
ggccaggaag gtgtggcagc cgactggcc gcctgcaaaa tctcaaaga gatgtcgac 1680
ctggagacgg agggcgaggg gggccgagcc acgcgcgagg cgaaatacga gcggctggcc 1740
cttgacctct tctccgagtg ctacagcaac agtgaggccc gcgccttcgc cctgctggtg 1800
cgccggaacc gctgctggag caagaccacc tgccctgcacc tggccaccga ggctgacgcc 1860
aaggccttct ttgcccacga cggcggttcag gccttctctga ccaggatctg gtggggggac 1920
atggccgcag gcacgcccac cctgcggctg ctaggagcct tctctgccc cgccctcgtc 1980
tataccaacc tcatcacctt cagtgaggaa gtcctcctga ggacaggcct ggaggacctg 2040
caggacctgg acagcctgga caccgagaag agcccgtgt atggcctgca gagccgggtg 2100
gaggagctgg tggaggcgcc gagggtcag ggtgaccgag gccacgtgc tgtcttcctg 2160
ctcacacgct ggcggaatt ctggggcgct cccgtgactg tgttcctggg gaacgtggtc 2220
atgtacttcg ctttctctt cctgttcacc tacgtcctgc tgggtggactt caggccgccc 2280
ccccagggcc cctcagggcc cgaggtcacc ctctacttct ggggtctttac gctggtgctg 2340
gaggaaatcc ggcagggtct cttcacagac gaggacacac acctggtgaa gaagttcaca 2400
ctgtatgtgg gggacaactg gaacaagtgt gacatgggtg ccacttctct gttcatcgtg 2460
ggtgtcacct gcaggatgct gccgtcggcg tttgaggctg gccgcacggt cctcgccatg 2520
gacttcattg tgttcacgct gcggctgatc catatctttg ccatacacia gcagctgggc 2580
cccaagatca tcgtggtaga gcgcctgatg aaggacgtct tcttcttct cttctttctg 2640
agcgtgtggc tcgtggccta cgggtgtcacc acccaggcgc tgctgcaccc ccatgacggc 2700
cgcttgaggt ggatcttccg cggggtgtct taccggccct acctgcagat cttcggccag 2760
atcccaactg acgagattga tgaagcccg gtgaactgct ccaccacccc actgctgctg 2820
gaggactcac catctgccc cagcctctat gccaaactggc tggtcactct cctgctggtc 2880
accttctctg tggtcaccaa tgtgctgctc atgaacctgc tcatcgccat gttcagctac 2940
acgttcagg tgggtcaggg caacgcagac atgttctgga agttccaggc ctacaacctg 3000
attgtggagt accacgagcg ccccgccctg gcccgccct tcatcctgct cagccacctg 3060
agcctgacgc tccgcccgggt cttcaagaag gaggctgagc acaagcggga gcacctggag 3120
agagacctgc cagaccccct ggaccagaag gtcgtcacct gggagacagt ccagaaggag 3180
aacttctgga gcaagatgga gaagcggagg agggacagcg agggggaggt gctgcggaaa 3240
accgcccaca gagtggactt cattgccaag tacctcgggg ggctgagaga gcaagaaaag 3300
cgcacaaagt gtctggagtc acagatcaac tactgctcgg tgctcgtgtc ctccgtggct 3360
gacgtgctgg cccaggggtg cggcccccgg agctctcagc actgtggcga gggaagccag 3420
ctggtggctg ctgaccacag aggtggttta gatggctggg aacaaccgg ggctggccag 3480
cctccctcgg acacatga 3498

```

<210> 4
<211> 1165
<212> PRT
<213> Human

```

<400> 4
Met Gln Asp Val Gln Gly Pro Arg Pro Gly Ser Pro Gly Asp Ala Glu
1          5          10          15
Asp Arg Arg Glu Leu Gly Leu His Arg Gly Glu Val Asn Phe Gly Gly
20          25          30
Ser Gly Lys Lys Arg Gly Lys Phe Val Arg Val Pro Ser Gly Val Ala
35          40          45
Pro Ser Val Leu Phe Asp Leu Leu Leu Ala Glu Trp His Leu Pro Ala
50          55          60
Pro Asn Leu Val Val Ser Leu Val Gly Glu Glu Gln Pro Phe Ala Met
65          70          75          80
Lys Ser Trp Leu Arg Asp Val Leu Arg Lys Gly Leu Val Lys Ala Ala

```

Lys	Ser	Trp	Leu	Arg	Asp	Val	Leu	Arg	Lys	Gly	Leu	Val	Lys	Ala	Ala	
			85						90					95		
Gln	Ser	Thr	Gly	Ala	Trp	Ile	Leu	Thr	Ser	Ala	Leu	Arg	Val	Gly	Leu	
			100					105					110			
Ala	Arg	His	Val	Gly	Gln	Ala	Val	Arg	Asp	His	Ser	Leu	Ala	Ser	Thr	
		115					120					125				
Ser	Thr	Lys	Val	Arg	Val	Val	Ala	Val	Gly	Met	Ala	Ser	Leu	Gly	Arg	
	130					135					140					
Val	Leu	His	Arg	Arg	Ile	Leu	Glu	Glu	Ala	Gln	Glu	Asp	Phe	Pro	Val	
145					150					155					160	
His	Tyr	Pro	Glu	Asp	Gly	Gly	Ser	Gln	Gly	Pro	Leu	Cys	Ser	Leu		
				165				170					175			
Asp	Ser	Asn	Leu	Ser	His	Phe	Ile	Leu	Val	Glu	Pro	Gly	Pro	Pro	Gly	
			180					185					190			
Lys	Gly	Asp	Gly	Leu	Thr	Glu	Leu	Arg	Leu	Arg	Leu	Glu	Lys	His	Ile	
		195					200					205				
Ser	Glu	Gln	Arg	Ala	Gly	Tyr	Gly	Gly	Thr	Gly	Ser	Ile	Glu	Ile	Pro	
	210					215					220					
Val	Leu	Cys	Leu	Leu	Val	Asn	Gly	Asp	Pro	Asn	Thr	Leu	Glu	Arg	Ile	
225						230				235					240	
Ser	Arg	Ala	Val	Glu	Gln	Ala	Ala	Pro	Trp	Leu	Ile	Leu	Val	Gly	Ser	
			245						250					255		
Gly	Gly	Ile	Ala	Asp	Val	Leu	Ala	Ala	Leu	Val	Asn	Gln	Pro	His	Leu	
		260						265					270			
Leu	Val	Pro	Lys	Val	Ala	Glu	Lys	Gln	Phe	Lys	Glu	Lys	Phe	Pro	Ser	
		275					280					285				
Lys	His	Phe	Ser	Trp	Glu	Asp	Ile	Val	Arg	Trp	Thr	Lys	Leu	Leu	Gln	
	290					295					300					
Asn	Ile	Thr	Ser	His	Gln	His	Leu	Leu	Thr	Val	Tyr	Asp	Phe	Glu	Gln	
305					310					315					320	
Glu	Gly	Ser	Glu	Glu	Leu	Asp	Thr	Val	Ile	Leu	Lys	Ala	Leu	Val	Lys	
			325						330					335		
Ala	Cys	Lys	Ser	His	Ser	Gln	Glu	Pro	Gln	Asp	Tyr	Leu	Asp	Glu	Leu	
			340					345					350			
Lys	Leu	Ala	Val	Ala	Trp	Asp	Arg	Val	Asp	Ile	Ala	Lys	Ser	Glu	Ile	
		355					360					365				
Phe	Asn	Gly	Asp	Val	Glu	Trp	Lys	Ser	Cys	Asp	Leu	Glu	Glu	Val	Met	
	370					375					380					
Val	Asp	Ala	Leu	Val	Ser	Asn	Lys	Pro	Glu	Phe	Val	Arg	Leu	Phe	Val	
385					390					395					400	
Asp	Asn	Gly	Ala	Asp	Val	Ala	Asp	Phe	Leu	Thr	Tyr	Gly	Arg	Leu	Gln	
			405					410					415			
Glu	Leu	Tyr	Arg	Ser	Val	Ser	Arg	Lys	Ser	Leu	Leu	Phe	Asp	Leu	Leu	
		420						425					430			
Gln	Arg	Lys	Gln	Glu	Glu	Ala	Arg	Leu	Thr	Leu	Ala	Gly	Leu	Gly	Thr	
		435					440					445				
Gln	Gln	Ala	Arg	Glu	Pro	Pro	Ala	Gly	Pro	Pro	Ala	Phe	Ser	Leu	His	
	450					455					460					
Glu	Val	Ser	Arg	Val	Leu	Lys	Asp	Phe	Leu	Gln	Asp	Ala	Cys	Arg	Gly	
465					470					475					480	
Phe	Tyr	Gln	Asp	Gly	Arg	Pro	Gly	Asp	Arg	Arg	Arg	Ala	Glu	Lys	Gly	
			485						490					495		
Pro	Ala	Lys	Arg	Pro	Thr	Gly	Gln	Lys	Trp	Leu	Leu	Asp	Leu	Asn	Gln	
		500						505					510			
Lys	Ser	Glu	Asn	Pro	Trp	Arg	Asp	Leu	Phe	Leu	Trp	Ala	Val	Leu	Gln	

		515					520					525					
Asn	Arg	His	Glu	Met	Ala	Thr	Tyr	Phe	Trp	Ala	Met	Gly	Gln	Glu	Gly		
530						535					540						
Val	Ala	Ala	Ala	Leu	Ala	Ala	Cys	Lys	Ile	Leu	Lys	Glu	Met	Ser	His		
545					550					555					560		
Leu	Glu	Thr	Glu	Ala	Glu	Ala	Ala	Arg	Ala	Thr	Arg	Glu	Ala	Lys	Tyr		
				565					570					575			
Glu	Arg	Leu	Ala	Leu	Asp	Leu	Phe	Ser	Glu	Cys	Tyr	Ser	Asn	Ser	Glu		
			580					585					590				
Ala	Arg	Ala	Phe	Ala	Leu	Leu	Val	Arg	Arg	Asn	Arg	Cys	Trp	Ser	Lys		
		595					600					605					
Thr	Thr	Cys	Leu	His	Leu	Ala	Thr	Glu	Ala	Asp	Ala	Lys	Ala	Phe	Phe		
610						615					620						
Ala	His	Asp	Gly	Val	Gln	Ala	Phe	Leu	Thr	Arg	Ile	Trp	Trp	Gly	Asp		
625					630					635					640		
Met	Ala	Ala	Gly	Thr	Pro	Ile	Leu	Arg	Leu	Leu	Gly	Ala	Phe	Leu	Cys		
				645					650					655			
Phe	Ala	Leu	Val	Tyr	Thr	Asn	Leu	Ile	Thr	Phe	Ser	Glu	Glu	Ala	Pro		
			660					665					670				
Leu	Arg	Thr	Gly	Leu	Glu	Asp	Leu	Gln	Asp	Leu	Asp	Ser	Leu	Asp	Thr		
		675					680					685					
Glu	Lys	Ser	Pro	Leu	Tyr	Gly	Leu	Gln	Ser	Arg	Val	Glu	Glu	Leu	Val		
690						695					700						
Glu	Ala	Pro	Arg	Ala	Gln	Gly	Asp	Arg	Gly	Pro	Arg	Ala	Val	Phe	Leu		
705					710					715					720		
Leu	Thr	Arg	Trp	Arg	Lys	Phe	Trp	Gly	Ala	Pro	Val	Thr	Val	Phe	Leu		
				725					730					735			
Gly	Asn	Val	Val	Met	Tyr	Phe	Ala	Phe	Leu	Phe	Leu	Phe	Thr	Tyr	Val		
			740					745					750				
Leu	Leu	Val	Asp	Phe	Arg	Pro	Pro	Gln	Gly	Pro	Ser	Gly	Pro	Glu			
		755					760				765						
Val	Thr	Leu	Tyr	Phe	Trp	Val	Phe	Thr	Leu	Val	Leu	Glu	Glu	Ile	Arg		
770						775					780						
Gln	Gly	Phe	Phe	Thr	Asp	Glu	Asp	Thr	His	Leu	Val	Lys	Lys	Phe	Thr		
785					790					795					800		
Leu	Tyr	Val	Gly	Asp	Asn	Trp	Asn	Lys	Cys	Asp	Met	Val	Ala	Ile	Phe		
				805					810					815			
Leu	Phe	Ile	Val	Gly	Val	Thr	Cys	Arg	Met	Leu	Pro	Ser	Ala	Phe	Glu		
			820					825					830				
Ala	Gly	Arg	Thr	Val	Leu	Ala	Met	Asp	Phe	Met	Val	Phe	Thr	Leu	Arg		
		835					840					845					
Leu	Ile	His	Ile	Phe	Ala	Ile	His	Lys	Gln	Leu	Gly	Pro	Lys	Ile	Ile		
850						855					860						
Val	Val	Glu	Arg	Met	Met	Lys	Asp	Val	Phe	Phe	Phe	Leu	Phe	Phe	Leu		
865					870					875					880		
Ser	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Thr	Thr	Gln	Ala	Leu	Leu	His		
				885					890					895			
Pro	His	Asp	Gly	Arg	Leu	Glu	Trp	Ile	Phe	Arg	Arg	Val	Leu	Tyr	Arg		
			900					905					910				
Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro	Leu	Asp	Glu	Ile	Asp	Glu		
		915					920					925					
Ala	Arg	Val	Asn	Cys	Ser	Thr	His	Pro	Leu	Leu	Leu	Glu	Asp	Ser	Pro		
930						935						940					
Ser	Cys	Pro	Ser	Leu	Tyr	Ala	Asn	Trp	Leu	Val	Ile	Leu	Leu	Leu	Val		
945					950					955					960		
Thr	Phe	Leu	Leu	Val	Thr	Asn	Val	Leu	Leu	Met	Asn	Leu	Leu	Ile	Ala		
				965				970						975			

Met	Phe	Ser	Tyr	Thr	Phe	Gln	Val	Val	Gln	Gly	Asn	Ala	Thr	Met	Phe
			980						985					990	
Trp	Lys	Phe	Gln	Arg	Tyr	Asn	Leu	Ile	Val	Glu	Tyr	His	Glu	Arg	Pro
		995					1000					1005			
Ala	Leu	Ala	Pro	Pro	Phe	Ile	Leu	Leu	Ser	His	Leu	Ser	Leu	Thr	Leu
	1010					1015					1020				
Arg	Arg	Val	Phe	Lys	Lys	Glu	Ala	Glu	His	Lys	Arg	Glu	His	Leu	Glu
1025					1030					1035					1040
Arg	Asp	Leu	Pro	Asp	Pro	Leu	Asp	Gln	Lys	Val	Val	Thr	Trp	Glu	Thr
			1045						1050					1055	
Val	Gln	Lys	Glu	Asn	Phe	Leu	Ser	Lys	Met	Glu	Lys	Arg	Arg	Arg	Asp
		1060						1065				1070			
Ser	Glu	Gly	Glu	Val	Leu	Arg	Lys	Thr	Ala	His	Arg	Val	Asp	Phe	Ile
	1075						1080					1085			
Ala	Lys	Tyr	Leu	Gly	Gly	Leu	Arg	Glu	Gln	Glu	Lys	Arg	Ile	Lys	Cys
	1090					1095					1100				
Leu	Glu	Ser	Gln	Ile	Asn	Tyr	Cys	Ser	Val	Leu	Val	Ser	Ser	Val	Ala
1105					1110					1115					1120
Asp	Val	Leu	Ala	Gln	Gly	Gly	Gly	Pro	Arg	Ser	Ser	Gln	His	Cys	Gly
			1125					1130						1135	
Glu	Gly	Ser	Gln	Leu	Val	Ala	Ala	Asp	His	Arg	Gly	Gly	Ile	Asp	Gly
		1140						1145				1150			
Trp	Glu	Gln	Pro	Gly	Ala	Gly	Gln	Pro	Pro	Ser	Asp	Thr			
	1155						1160					1165			